

## SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Method for identifying compounds that modulate sister chromatid separation

<130> 0652.2290001

<140> To be assigned

<141> Herewith

<150> EP 01 101 252.3

<151> 2001-01-19

<150> US 60/297,440

<151> 2001-06-13

<160> 8

<170> PatentIn Ver. 2.1

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<211> 6668

<212> DNA

<213> Homo sapiens

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Lys Ala Gln Lys His Arg Gly Ser Leu Glu Ile Ala Asp Gln Leu Gln	
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ggg ctg agc ctt cag gag atg cct gga gat gtc ccc ctg gcc cgc atc	5163
Gly Leu Ser Leu Gln Glu Met Pro Gly Asp Val Pro Leu Ala Arg Ile	
1660 1665 1670	
cag cgc ctc ttt tcc ttc agg gct ttg gaa tct ggc cac ttc ccc cag	5211
Gln Arg Leu Phe Ser Phe Arg Ala Leu Glu Ser Gly His Phe Pro Gln	
1675 1680 1685	
cct gaa aag gag agt ttc cag gag cgc ctg gct ctg atc ccc agt ggg	5259
Pro Glu Lys Glu Ser Phe Gln Glu Arg Leu Ala Leu Ile Pro Ser Gly	
1690 1695 1700 1705	
gtg act gtg tgt gtg ttg gcc ctg gcc acc ctc cag ccc gga acc gtg	5307
Val Thr Val Cys Val Leu Ala Leu Ala Thr Leu Gln Pro Gly Thr Val	
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Gly Asn Thr Leu Leu Thr Arg Leu Glu Lys Asp Ser Pro Pro Val	
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agt gtg cag att ccc act ggc cag aac aag ctt cat ctg cgt tca gtc	5403
Ser Val Gln Ile Pro Thr Gly Gln Asn Lys Leu His Leu Arg Ser Val	
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ctg aat gag ttt gat gcc atc cag aag gca cag aaa gag aac agc agc	5451
Leu Asn Glu Phe Asp Ala Ile Gln Lys Ala Gln Lys Glu Asn Ser Ser	
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tgt act gac aag cga gaa tgg tgg aca ggg cgg ctg gca ctg gac cac	5499
Cys Thr Asp Lys Arg Glu Trp Trp Thr Gly Arg Leu Ala Leu Asp His	
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agg atg gag gtt ctc atc gct tcc cta gag aag tct gtg ctg ggc tgc	5547
Arg Met Glu Val Leu Ile Ala Ser Leu Glu Lys Ser Val Leu Gly Cys	
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Trp Lys Gly Leu Leu Leu Pro Ser Ser Glu Glu Pro Gly Pro Ala Gln	

1805	1810	1815	
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cct gac cgc act ctg ctg Pro Asp Arg Thr Leu Leu 1835	aaa atc atg ctc agt Lys Ile Met Leu Ser 1840	ggt gcc ggt gcc ctc Gly Ala Gly Ala Leu 1845	5691
acc cct cag gac att cag Thr Pro Gln Asp Ile 1850	gcc ctg gcc tac ggg Ala Leu Ala Tyr Gly 1855	ctg tgc cca acc cag Leu Cys Pro Thr Gln 1860	5739
cca gag cga gcc cag Pro Glu Arg Ala Gln 1870	gag ctc ctg aat gag Glu Leu Leu Asn Glu 1875	gca gta gga cgt cta cag Ala Val Gly Arg Leu Gln 1880	5787
ggc ctg aca gta cca agc Gly Leu Thr Val Pro 1885	aat agc cac ctt gtc Ser Asn Ser His Leu 1890	gtc ttg gtc cta gac aag Val Leu Val Leu Asp Lys 1895	5835
gac ttg cag aag ctg ccg Asp Leu Gln Lys Leu 1900	ctg tgg gaa agc atg Trp Glu Ser Met Pro 1905	ccc agc ctc caa gca ctg Ser Leu Gln Ala Leu 1910	5883
cct gtc acc cgg ctg ccc Pro Val Thr Arg Leu 1915	ccc tcc ttc cgc ttc Pro Ser Phe Arg Phe 1920	cta ctc agc tac tcc atc Leu Leu Ser Tyr Ser Ile 1925	5931
atc aaa gag tat ggg gcc Ile Lys Glu Tyr Gly 1930	tcg cca gtg ctg agt Ala Ser Pro Val Leu 1935	caa ggg gtg gat cca Gln Gly Val Asp Pro 1940	5979
cga agt acc ttc tat gtc Arg Ser Thr Phe Tyr 1950	ctg aac cct cac aat Leu Asn Pro His Asn 1955	aac ctg tca agc aca Asn Leu Ser Ser Thr 1960	6027
gag gag caa ttt cga gcc Glu Glu Gln Phe Arg 1965	aat ttc agc agt gaa Asn Phe Ser Ser Glu 1970	gct ggc tgg aga gga Ala Gly Trp Arg Gly 1975	6075
gtg gtt ggg gag gtg cca Val Val Gly Glu Val 1980	aga cct gaa cag gtg Pro Arg Pro Glu Gln 1985	cag gaa gcc ctg aca Val Gln Glu Ala Leu 1990	6123
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ctt gat ggg cag gct gtc Leu Asp Gly Gln Ala 2010	ctg cgg ctg agc tgt Leu Arg Leu Ser Cys 2015	cgg gca gtg gcc ctg Arg Ala Val Ala Leu 2020	6219
ctg ttt ggc tgt agc agt Leu Phe Gly Cys Ser 2030	gcg gcc ctg gct gtg Ala Ala Leu Ala Val 2035	cat gga aac ctg gag His Gly Asn Leu Glu 2040	6267
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Pro	Pro	Ala	Gly	Phe	Pro	Ser	Ser	Arg	Ser	Asp	Ala	Glu	Arg	Arg	Gln	
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Ala	Cys	Asp	Gly	Tyr	Leu	Val	Ser	Thr	Pro	Gln	Arg	Pro	Pro	Leu	Tyr	
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Val	Gln	Cys	Ser	Arg	Glu	Ala	Ala	Pro	Gln	Asp	Tyr	Glu	Ala	Val	Ala	
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Arg	Gly	Ser	Phe	Ser	Leu	Leu	Trp	Lys	Gly	Ala	Glu	Ala	Leu	Leu	Glu	
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Arg	Arg	Ala	Ala	Phe	Ala	Ala	Arg	Leu	Lys	Ala	Leu	Ser	Phe	Leu	Val	
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Pro	Thr	Ala 195	Cys	Arg	Ala	Val	Ala 200	Ala	His	Gln	Leu	Phe 205	Asp	Ala	Ser
Gly	His 210	Gly	Leu	Asn	Glu	Ala 215	Asp	Ala	Asp	Phe	Leu 220	Asp	Asp	Leu	Leu
Ser 225	Arg	His	Val	Ile	Arg 230	Ala	Leu	Val	Gly	Glu 235	Arg	Gly	Ser	Ser	Ser 240
Gly	Leu	Leu	Ser	Pro 245	Gln	Arg	Ala	Leu	Cys 250	Leu	Leu	Glu	Leu	Thr 255	Leu
Glu	His	Cys 260	Arg	Arg	Phe	Cys	Trp	Ser 265	Arg	His	His	Asp	Lys 270	Ala	Ile
Ser	Ala	Val 275	Glu	Lys	Ala	His	Ser 280	Tyr	Leu	Arg	Asn	Thr 285	Asn	Leu	Ala
Pro	Ser 290	Leu	Gln	Leu	Cys	Gln 295	Leu	Gly	Val	Lys	Leu 300	Leu	Gln	Val	Gly
Glu 305	Glu	Gly	Pro	Gln	Ala 310	Val	Ala	Lys	Leu	Leu 315	Ile	Lys	Ala	Ser	Ala 320
Val	Leu	Ser	Lys	Ser 325	Met	Glu	Ala	Pro	Ser 330	Pro	Pro	Leu	Arg	Ala 335	Leu
Tyr	Glu	Ser	Cys 340	Gln	Phe	Phe	Leu	Ser 345	Gly	Leu	Glu	Arg	Gly 350	Thr	Lys
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Gly 385	Ser	Ser	Lys	Gln	Gln 390	Gln	Ser	Phe	Leu	Gln 395	Met	Tyr	Phe	Gln	Gly 400
Leu	His	Leu	Tyr	Thr 405	Val	Val	Val	Tyr	Asp 410	Phe	Ala	Gln	Gly	Cys 415	Gln
Ile	Val	Asp	Leu 420	Ala	Asp	Leu	Thr	Gln 425	Leu	Val	Asp	Ser	Cys 430	Lys	Ser
Thr	Val	Val 435	Trp	Met	Leu	Glu	Ala 440	Leu	Glu	Gly	Leu	Ser 445	Gly	Gln	Glu
Leu	Thr 450	Asp	His	Met	Gly	Met 455	Thr	Ala	Ser	Tyr	Thr 460	Ser	Asn	Leu	Ala
Tyr 465	Ser	Phe	Tyr	Ser	His 470	Lys	Leu	Tyr	Ala	Glu 475	Ala	Cys	Ala	Ile	Ser 480
Glu	Pro	Leu	Cys	Gln 485	His	Leu	Gly	Leu	Val 490	Lys	Pro	Gly	Thr	Tyr 495	Pro
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 Leu Trp Leu Ala Ala Leu Gln Pro Cys Ser Pro Glu His Met Ala Glu  
 530 535 540  
 Pro Val Thr Phe Trp Val Arg Val Lys Met Asp Ala Ala Arg Ala Gly  
 545 550 555 560  
 Asp Lys Glu Leu Gln Leu Lys Thr Leu Arg Asp Ser Leu Ser Gly Trp  
 565 570 575  
 Asp Pro Glu Thr Leu Ala Leu Leu Leu Arg Glu Glu Leu Gln Ala Tyr  
 580 585 590  
 Lys Ala Val Arg Ala Asp Thr Gly Gln Glu Arg Phe Asn Ile Ile Cys  
 595 600 605  
 Asp Leu Leu Glu Leu Ser Pro Glu Glu Thr Pro Ala Gly Ala Trp Ala  
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 Arg Ala Thr His Leu Val Glu Leu Ala Gln Val Leu Cys Tyr His Asp  
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 Phe Thr Gln Gln Thr Asn Cys Ser Ala Leu Asp Ala Ile Arg Glu Ala  
 645 650 655  
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 660 665 670  
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 Ala Pro Gly Asn Leu Glu Glu Phe Glu Val Asn Asp Leu Asn Tyr Glu  
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 Asp Lys Leu Gln Glu Asp Arg Phe Leu Tyr Ser Asn Ile Ala Phe Asn  
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 755 760 765  
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 770 775 780  
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 Ile Val Ser Glu Arg Leu Lys Asp His Ser Lys Ala Ala Gly Ser Ser  
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 Cys His Ile Thr Gln Leu Leu Leu Thr Leu Gly Cys Pro Ser Tyr Ala  
 820 825 830  
 Gln Leu His Leu Glu Glu Ala Ala Ser Ser Leu Lys His Leu Asp Gln

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Ser	Gln	Leu	Tyr	Trp	Thr	His	Gln	Lys	Val	Thr	Lys	Gly	Val	Ser	Leu
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Leu	Leu	Ser	Val	Leu	Arg	Asp	Pro	Ala	Leu	Gln	Lys	Ser	Ser	Lys	Ala
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Trp	Tyr	Leu	Leu	Arg	Val	Gln	Val	Leu	Gln	Leu	Val	Ala	Ala	Tyr	Leu
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Ser	Leu	Pro	Ser	Asn	Asn	Leu	Ser	His	Ser	Leu	Trp	Glu	Gln	Leu	Cys
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Ala	Gln	Gly	Trp	Gln	Thr	Pro	Glu	Ile	Ala	Leu	Ile	Asp	Ser	His	Lys
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 Ser Cys Cys Thr Thr Gln Leu Phe Ala Ser Ser Trp Gly Trp Gln Pro  
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 Pro Leu Ile Lys Ser Val Pro Gly Ser Glu Pro Ser Lys Thr Gln Gly  
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 Arg Ala Lys Lys Val Ala Ser Arg His Cys Glu Glu Arg Arg Pro Gln  
 1460 1465 1470  
 Arg Ala Ser Asp Gln Ala Arg Pro Gly Pro Glu Ile Met Arg Thr Ile  
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 Pro Glu Glu Glu Leu Thr Asp Asn Trp Arg Lys Met Ser Phe Glu Ile  
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Leu Arg Gly Ser Asp Gly Glu Asp Ser Ala Ser Gly Gly Lys Thr Pro  
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 Ala Pro Gly Pro Glu Ala Ala Ser Gly Glu Trp Glu Leu Leu Arg Leu  
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 Thr Gly Leu Ser Thr Leu Asp Ser Ile Cys Asp Ser Leu Ser Val Ala  
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Ile Met Leu Ser Gly Ala Gly Ala Leu Thr Pro Gln Asp Ile Gln Ala  
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 Leu Asn Glu Ala Val Gly Arg Leu Gln Gly Leu Thr Val Pro Ser Asn  
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 Glu Ser Met Pro Ser Leu Gln Ala Leu Pro Val Thr Arg Leu Pro Ser  
 1905 1910 1915 1920  
 Phe Arg Phe Leu Leu Ser Tyr Ser Ile Ile Lys Glu Tyr Gly Ala Ser  
 1925 1930 1935  
 Pro Val Leu Ser Gln Gly Val Asp Pro Arg Ser Thr Phe Tyr Val Leu  
 1940 1945 1950  
 Asn Pro His Asn Asn Leu Ser Ser Thr Glu Glu Gln Phe Arg Ala Asn  
 1955 1960 1965  
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 1970 1975 1980  
 Pro Glu Gln Val Gln Glu Ala Leu Thr Lys His Asp Leu Tyr Ile Tyr  
 1985 1990 1995 2000  
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<223> Description of Artificial Sequence:primer

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